BOOK REVIEWS

DAN GRAUR and WEN-HSIUNG LI. 2000. **Fundamentals of Molecular Evolution, Second edition.** (ISBN 0-87893-266-6, pbk.). Sinauer Associates, Inc., PO Box 407, 23 Plumtree Road, Sunderland, MA 01375 U.S.A. (Orders: Internet: publish@sinauer.com, www.sinauer.com, 413-549-1118 fax). $48.95, pbk., 482 pp., 7" × 9".

Having been trained in biosystematics and comparative secondary chemistry, I feel a bit like the driver of an old 70s model car who has just been left behind in the dust of a new sporty model, the molecular systematics model, that is. Hence, I approached reviewing this book from the standpoint of whether it could bring me up to date in my understanding of molecular biology and how the data are applied to systematics.

After reading this book, I do feel more comfortable discussing introns, reverse transcription, transposons, and so on. In that sense, the book succeeded in passing the test of teaching me. However, the explanations in some sections took several readings. This was particularly true for concepts that, introduced early in the book, were the basis for models or for more complex concepts later in the book (e.g., replication of leading vs. lagging strands; Holliday structures and heteroduplexes; calculation of mutation and/or substitution rates).

Not only the title but also the tenor of the introduction suggest that the book assumes the reader has a basic understanding of molecular biology and genetics. Presumably, the main goal of this book is to familiarize graduate students and tangential professionals to be able to read and understand the primary literature and to provide them with the tools for learning research techniques. However, it is not a "cookbook" of techniques in molecular systematics and population genetics. Unfortunately, the book also tries to be a primer to the beginner. In attempting to cover so many basic topics, the primer part becomes shallow and inaccurate. For example, the first chapter begins with an explanation of DNA. In the second paragraph, the four bases are equated with nucleotides:

Each chain is a linear polynucleotide consisting of four kinds of nucleotides. There are two purines, adenine (A) and guanine (G), and two pyrimidines, thymine (T) and cytosine (C).

Before the term "base" is explained, the concept of canonical base pairs is presented.

This brings up another weakness. There is no glossary. Certain words are boldface in both the text and index. These words are considered to be "defined" where first presented in the text. Often, this definition must be gleaned from context only.

Writers of conceptually oriented books need to be careful to present assumptions that underlie the various concepts; for the most part, these authors have succeeded. However, they were not always aware of their assumptions, especially of their bias of the supremacy of molecular methods over more "traditional" ones, as is evident on page 3:

"... the introduction of molecular methods has undoubtedly put evolution on a much more solid footing, and has turned it into a science in which relevant parameters are measured, counted, or computed from empirical data, and theories are tested against objective reality.

Such statements reveal that the authors really do not understand that molecular data faces many of the same limitations (indeed more severe limitations in the case of homoplasious base differences) as does organismal data when both data types are subjected to algorithms of population genetics and cladistics. Likewise, the authors seem (to me) to be making the assumption that the genome contains all necessary information for controlling all developmental pathways differentiating taxa, whereas recent research is also pointing to the proteinome and maternal inheritance as major factors, as well.

As explained in the introduction, the book focuses on instructing in two major areas: 1) molecular evolution as hypotheses of phylogeny and character transformations; and 2) molecular evolution as hypotheses of cause and effect of differences among organisms. The topics related to the two major areas are presented in eight rather long chapters.

Chapter One, where basic terms and concepts are introduced, suffers many of the problems already mentioned.

Chapter Two introduces concepts of population genetics, especially rates of gene substitution under differing assumptions and conditions. The connection between populational studies and nucleotide substitutional differences among species and higher groups is poorly developed. The ongoing controversy between the hypotheses of the neo-Darwinian selectionists and neutral mutation advocates is well covered.

In **Chapter Three**, the authors outlined the evolutionary assumptions made in comparing nucleotide sequences among individual organisms and taxa. Methods for aligning sequences, from visual inspection to computer algorithms, are covered.

Based on these assumptions, **Chapter Four** shows how sequence comparisons are used to draw conclusions about the mechanisms and rates of nucleotide substitution. Because some sites and regions show greater differences than do other regions, an important part of the chapter examines mechanisms that might explain these nonrandom biases.

For the systematist, **Chapter Five** contains the most meat—the use of nucleotide sequence data to construct hypothetical phylogenies. Not only does it introduce the vocabulary of phylogenetics, but also covers theoretical problems, as well. Presentation of distance measures and the mathematics for UPGMA (unweighted pair group method with arithmetic means) of distance measures, transformed distance methods (true parsimony), neighbors-relation and neighbor-joining methods, and minimum spanning trees figures prominently in the chapter. I think the book could have been improved if the authors had given (in appendices) step-by-step examples to work through by hand for these different methods. Because the math of computerized parsimony algorithms (exhaustive and heuristic searches and tree comparisons) and maximum likelihood is very complicated, only the description of these methods is given. Also included are rooting methods, estimating divergence time, and tree reliability assessments (e.g., bootstrap). Several examples from recent studies were provided (human-ape; cetaceans; angiosperm origins; tree-of-life) to compare the strengths of the various analytical methods.

Looking beyond point mutations, **Chapter Six** examines duplication and modification of gene segments, especially pseudogenes, alternative pathways for producing new functions, and the lack of independent evolution of duplicated segments within species (so-called concerted evolution). The concept of evolution by "jumping genes," i.e., insertion or deletion of transposable elements, including both transposition and retroposition, is covered in **Chapter Seven.** Here the authors give a rather complete account of retrosequences, retroviruses, retroposons, and related sequences. I found the detailed explanations of LINEs and SINEs (long and short interspersed repetitive elements) to be helpful. Lateral gene transfer among unrelated species is an associated concept of special interest: can it account for discontinuity in the taxonomic distribution of isolated genetic sequences?

Chapter Eight relates attempts to account for traditional chromosomal differences at the molecular level. That is, what happens to the genome after polyploidization, what is heterochromatin, and why are there vast differences in sizes of genomes of diverse organism? Also two appendices provide additional background for those unfamiliar with 1) the geologic column, geologic history, and current species diversity; and 2) mathematical probabilities.

For the goals the authors have set for themselves, I would give the book a grade of "B." If other books that do a better job are not available in this niche, then, for the taxonomist needing a better understanding of molecular systematics, it is worth the investment.—*Roger W. Sanders, Associate Collections Manager, Botanical Research Institute of Texas, 509 Pecan Street, Fort Worth, TX 76102-4060, U.S.A., rsanders@brit.org.*